Complete if Known Substitute for form 1449A/PTO 10/823,784 Application Number **INFORMATION DISCLOSURE** April 14, 2004 Filing Date STATEMENT BY APPLICANT Karen UHLMANN et al First Named Inventor **Group Art Unit** (use as many sheets as necessary) **Examiner Name** of 3 Attomey Docket Number UHLMANN =1A Sheet

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		OTHER PRIOR ART - NON PATENT LITERATURE DOCUMENTS						
Examiner Cite Initiats* No.1		Include name of the author (in CAPITAL LETTERS), title of article (when appropriate), title of the item (book, magazine, journal, serial, symposium, catalog, etc.), date, page(s), volume-issue number(s), publisher, city and/or country where published						
08 M		ANTHONY, et al, "Mutation and methylation analysis of the transforming growth factor β receptor II gene in polycythaemia vera", British Journal of Haematology. (2001) 115:872-880.						
1	AB	BALOG, et al, "Parallel assessment of CpG methylation by two-color hybridization with oligonucleotide arrays", Analytical Biochemistry (20020) 309:301-310.	1					
	AC	BAUMER, et al, "A novel MSP/DHPLC method for the investigation of the methylation status of imprinted genes enables the molecular detection of low cell mosaicisms", Human Mutation (2001), 17:423-430.						
	AD	BIRD, Adrian and Edwin Southern, "Use of restriction enzymes to study Eurkaryotic DNA methylation: I. The methylation pattern in ribosomal DNA from <i>Xenopus laevis</i> ", J. Mol. Biol. (1978) 111:27-47.						
	AE	CEDER, et al, "Direct detection of methylation cytosine in DNA by use of the restriction enzyme Msp1", Nucleic Acids Research (1979) 6(6):2125-2132.						
	AF	CHURCH, George. and Walter Gilbert, "Genomic sequencing", Proc. Natl. Acad. Sci. USA (April 1984), 81:1991-1995.						
	AG	DAHL, Christina and Per Guldberg, "DNA methylation analysis techniques", Biogerontology (2003), 4:233-250.						
\prod	АН	DENG, et al, "Simultaneous detection of CpG methylation and single nucleotide polymorphism by denaturing high performance liquid chromatography", Nucleic Acids Research. (2002). 30(3):e13, (6pages).						
	AI	FRITZSCHE, et al, "The use of permanganate as a sequencing identification to 5-methylcytosine residues in DNA", Nucleic Acids Research (1987). 15(14):5517-5528.						
	AJ	FRAGA, Mario and Manel Esteller, "DNA methylation: A profile of methods and applications", BioTechniques (September 2002). 33:632-649.						
	AK	FROMMER, et al, "A genomic sequencing protocol that yields a positive display of 5-methylcytosine residues in individual DNA strands", Proc. Natl. Acad. Sci. USA (March 1992), 89:1827-1831.						
V	AL	FUKUHARA, et al, "Use of the polymerase chain reaction to detect hypermethylation in the calcitonin gene. A new, sensitive approach to monitor tumor cells in acute myelogenous leukemia", Leukemia Research. (1992). 16(10):1031-1040.						

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STAT	EMENT BY	ΔΡ	PLICANT	First Named Inventor	Karen UHLMANN et al		
VIAI		•		Group Art Unit	1645		
	(use as many sheets	as n	ecessary)	Examiner Name			
Sheet	2	of	3	Attorney Docket Number	UHLMANN =1A		

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0X	AM	EADS, et al, "MethyLight: a high-throughput assay to measure DNA methylation", Nucleic Acids Research. (2000). 28(8):e32:I-viii.	
i	AN	EL-MAARRI, et al, "A rapid quantitative, non-radioactive bisulfite-SnuPE-IP RP HPLC assay for methylation analyasis at specific CpG sites", Nucleic Acids Research (20020. 30(6):e25&4 pages).	
	AO	HEISKANEN, et al, "A novel methods to quantitate methylation of specific genomic regions", PCR Methods and Applications ((1994). 4:26-30.	
	AP	HERMAN, et al, "Methylation-specific PCR: A novel PCR assay for methylation status of CpG Islands", Proc. Natl. Acad. Sci. USA. (1996). 93:9821-9826.	
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	AR	LAIRD, Peter, "The power and the promise of DNA methylation markers", Cancer. (April 2003). 3:253-250.	
	AS	MARTIN, et al, "An analytical method for the detection of methylation differences at specific chromosomal loci using primer extension and ion pair reverse phase HPLC", Human Mutation. (2002). 20:305-311.	
	AT	McGREW, Michael, and Nadia Rosenthal, "Quantitation of genomic methylation using ligation-mediated PCR", BioTecniques. (1993). 15(4):722-729.	
	AU	OHMORI, et al, "Detection of 5-methycytosine in DNA sequence", Nucleic Acids Research. (1978). 5(5):1479- 1484.	
	AV	PAUL, Cheryl, and Susan Clark, "Cytosine methylation: Quantitation by automated genomic sequencing and GENESCAN TM analysis", BioTechniques. (1996). 21(1):126-133.	
	AW	PFEIFER, et al, "Genomic sequencing and methylation analysis by ligation mediated PCR", Science. (1989). 246:810-812.	:
\bigvee	AX	POGRIBNY, et al, "A sensitive new method for rapid detection of abnormal methylation patterns in global DNA and within CpG islands", Biochemical and Biophysical Research Communications. (1999). 262:624–628.	

Examiner Signature	amanda Shaw	Date Considered	2/22/06

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¹ Applicant's unique citation designation number (optional). ² Applicant is to place a check mark here if English language Translation is attached.

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d.	AY	BURRI, Nathalie, and Pascal Chaubert, "Complex methylation patterns analyzed by single-strand conformation polymorphism", BioTechniques. (1999). 26(2):232-234.							
Ì	AZ	REIN, et al, "Identifying 5-methylcytosine and related modifications in DNA genomes". Nucleic Acids Research. (1998). 26(10):2255-2264.							
	ВА	SADRI, Ramin, and Peter Hornsby, "Rapid analysis of DNA methylation using new restriction enzyme sites created by bisulfite modification", Nucleic Acids Research. (1996). 24(24):5058-5059.							
	ВВ	SANO, et al, "Identification of 5-methylcytosine in DNA fragments immobilized on nitrocellulose paper", Proc. Natl. Acad. Sci. USA. (June4 1980). 77(6):3581-3585.							
	ВС	STEIGERWALD, et al, "Ligation-mediated PCR improves the sensitivity of methylation analysis by restriction enzymes and detection of specific DNA strand breaks", Nucleic Acids Research. (1990). 18(6):1435-1439.							
	8D	WAALWIJK, C., and R.A. Flavell, "DNA methylation at a CCGG sequence in the large intron of the rabbit β-globi gne: Tissue-specific variations", Nucleic Acids Research. (December 1978). 5(12):4631-4641.							
	BE	WILSON, et al, "Genomic 5-methylcytosine determination by ³² P-postlabeling analysis", Analytical Biochemistry. (1986). 152:275-284.							
	BF	XIONG, Zhenggang, and eter Laird, "COBRA: A sensitive and quantitative DNA methylation assay", Nucleic Acids Research. (1997). 25(12):2532-2534.							
V	BG	YAN, et al, "Dissecting complex epigenetic alterations in breast cancer using CpG island microarrays", Cancer Research. (December 1, 2001). 61:8375-8380.							
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